

1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTCCTGGACAT  
M N K L L C C A L V F L D I  
42 CTCCATTAAGTGGACCACCCAGGAAACGTTTCCTCCAAAGT  
S I K W T T Q E T F P P K  
83 ACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGT  
Y L H Y D E E T S H Q L L C  
124 GACAAATGTCCTCCTGCTGCTACCTAACCTAAAACAACACTGTAC  
D K C P P G T Y L K Q H C T  
165 AGCAAAGTGGAAGACCGTGTGCGCCCCCTTGCCCCGACCACT  
A K W K T V C A P C P D H  
206 ACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATAC  
Y Y T D S W H T S D E C L Y  
247 TGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGA  
C S P V C K E L Q Y V K Q E  
288 GTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGGAAG  
C N R T H N R V C E C K E  
329 GCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGC  
G R Y L E I E F C L K H R S  
370 TGCCCTCCTGGATTGAGTGGTGTGCAAGCTGGAACCCCAGA  
C P P G F G V V Q A G T P E  
411 GCGAAATACAGTTTGCAAAAGATGTCCAGATGGGTTCCTCT  
R N T V C K R C P D G F F  
452 CAAATGAGACGTCATCTAAAGCACCCCTGTAGAAAACACACA  
S N E T S S K A P C R K H T  
493 AATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAA  
N C S V F G L L L T Q K G N  
534 TGCAACACACGACAACATATGTTCCGGAAACAGTGAATCAA  
S T V D N T C C C N C F C

2 / 5 MATCH WITH FIG. 1A

575 CTCAAAAATGTGGAATAGATGTTACCCCTGTGTGAGGAGGCA  
T Q K C G I D V T L C E E A  
616 TTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTG  
F F R F A V P T K F T P N W  
657 GCTTAGTGTCTTGGTAGACAATTTCCTGGCACCAAAGTAA  
L S V L V D N L P G T K V  
698 ACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCA  
N A E S V E R I K R Q H S S  
739 CAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCA  
Q E Q T F Q L L K L W K H Q  
780 AAACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATA  
N K D Q D I V K K I I Q D  
821 TTGACCTCTGTGAAAACAGCGTGCAGCGGCACATTGGACAT  
I D L C E N S V Q R H I G H  
862 GCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAG  
A N L T F E Q L R S L M E S  
903 CTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAA  
L P G K K V G A E D I E K  
944 CAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTG  
T I K A C K P S D Q I L K L  
985 CTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTT  
L S L W R I K N G D Q D T L  
1026 GAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACC  
K G L M H A L K H S K T Y  
1067 ACTTTCCACAAACTGTCACTCAGAGICTAAAGAAGACCAT  
H F P T N C H S E S K E D H  
1108 CAGGTTCCCTTCACAGCTTCACAATGTACAAATTGTATCAGA  
Q V P S Q L H N V Q I V S E  
1149 AGTTATTTTTAGAAATGATAGGTAA

# FIG. 2A

tnfr2.msf{TNFR2_LIKE}	1	.....MNKLL	CCALVFLDIS	IKWTTQETFP	P.....	KYLHYDEETS	50
tnfr2.msf{TNR2_HUMAN}		MAPVAVWAAL	AVGLELWAAA	HALPAQVAFT	PYAPEPGSTC	RLREYDQTA	
Consensus		-----L	---L-----	-----Q--F-	P-----	-----Y---T-	
tnfr2.msf{TNFR2_LIKE}	51	HQLLCDKCPP	GTYLKQHCTA	KWKTVCAPCP	DHYTDSWHT	SDECLYCSVP	100
tnfr2.msf{TNR2_HUMAN}		.QMCCSKCSP	GQHAKVFCTK	TSDTVCDSC	DSTYTQLWNW	VPECLSCGSR	
Consensus		-Q--C-KC-P	G---K--CT-	---TVC--C-	D--YT--W--	--ECL-C---	
tnfr2.msf{TNFR2_LIKE}	101	CKELQYVKQE	CNRTHNRVCE	CKEGRYLEIE	.....FCLK	HRSCPPGFGV	150
tnfr2.msf{TNR2_HUMAN}		CSSDQVETQA	CTREQNRICT	CRPGWYCAL	KQEGCRLCAP	LRKCRPGFGV	
Consensus		C---Q---Q-	C-R--NR-C-	C--G-Y----	-----C--	-R-C-PGFGV	
tnfr2.msf{TNFR2_LIKE}	151	VQAGTPERN	VCKRCPDGGF	SNETSSKAPC	RKHTNCSVFG	LLLTQKGNAT	200
tnfr2.msf{TNR2_HUMAN}		ARPGTETSDV	VCKPCAPGTF	SNTTSSTDIC	RPHQICNVVA	I....PGNAS	
Consensus		---GT-----	VCK-C--G-F	SN-TSS---C	R-H--C-V--	-----GNA-	
tnfr2.msf{TNFR2_LIKE}	201	HDNIC.....	.....	.....SGNSE	STQKCGIDVT	LCEEAFF...	250
tnfr2.msf{TNR2_HUMAN}		RDAVCTSTSP	TRSMAPGAVH	LPQPVSTRSQ	HTQPTPEPST	APSTSFLPM	
Consensus		-D--C-----	-----	-----S--S-	-TQ-----T	-----F----	

MATCH WITH FIG. 2B

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# FIG. 2B

MATCH WITH FIG. 2A

ifr2.msf(TNFR2\_LIKE) 251  
 ifr2.msf(TNFR2\_HUMAN) 300  
 Consensus

ifr2.msf(TNFR2\_LIKE) 301  
 ifr2.msf(TNFR2\_HUMAN) 350  
 Consensus

ifr2.msf(TNFR2\_LIKE) 351  
 ifr2.msf(TNFR2\_HUMAN) 400  
 Consensus

ifr2.msf(TNFR2\_LIKE) 401  
 ifr2.msf(TNFR2\_HUMAN) 450  
 Consensus

ifr2.msf(TNFR2\_LIKE) 451  
 ifr2.msf(TNFR2\_HUMAN) 475  
 Consensus

MATCH WITH FIG. 2C

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MATCH WITH FIG. 2B

FIG. 2C

Query: 38 QLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQYVKQEC 97  
 Q+ C KC PG + K CT TVC C D YT W+ ECL C C Q Q C  
 Sbjct: 29 QMCCSKCSPGQHAKVFC TKTS DTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQAC 88

Query: 98 NRTHNRVCECKEGRYLEIEFCLKHRS CPP 126  
 R NR+C C+ G Y + R C P  
 Sbjct: 89 TREQNRICRPGWYCALSKQEGCRLCAP 117

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Query: 118 CLKHRSCP PGFGVQAGTPERN TVCKRCPDGFNETSSKAPCRKHTNCSVFGL 171  
 C R C PGFGV + GT + VCK C G FSN TSS CR H C+V +  
 Sbjct: 115 CAPLRKCRPGFGVARPGTETSDV VCKPCAPGTFSTTSSTDICRPHQICNVVAI 168

Query: 177 GNATHDNICSGNS 189  
 GNA+ D +C+ S  
 Sbjct: 170 GNASMDAVCTSTS 182

Query: 363 SESKEDHQVP 372  
 SES +D QVP  
 Sbjct: 391 SESPKDEQVP 400

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